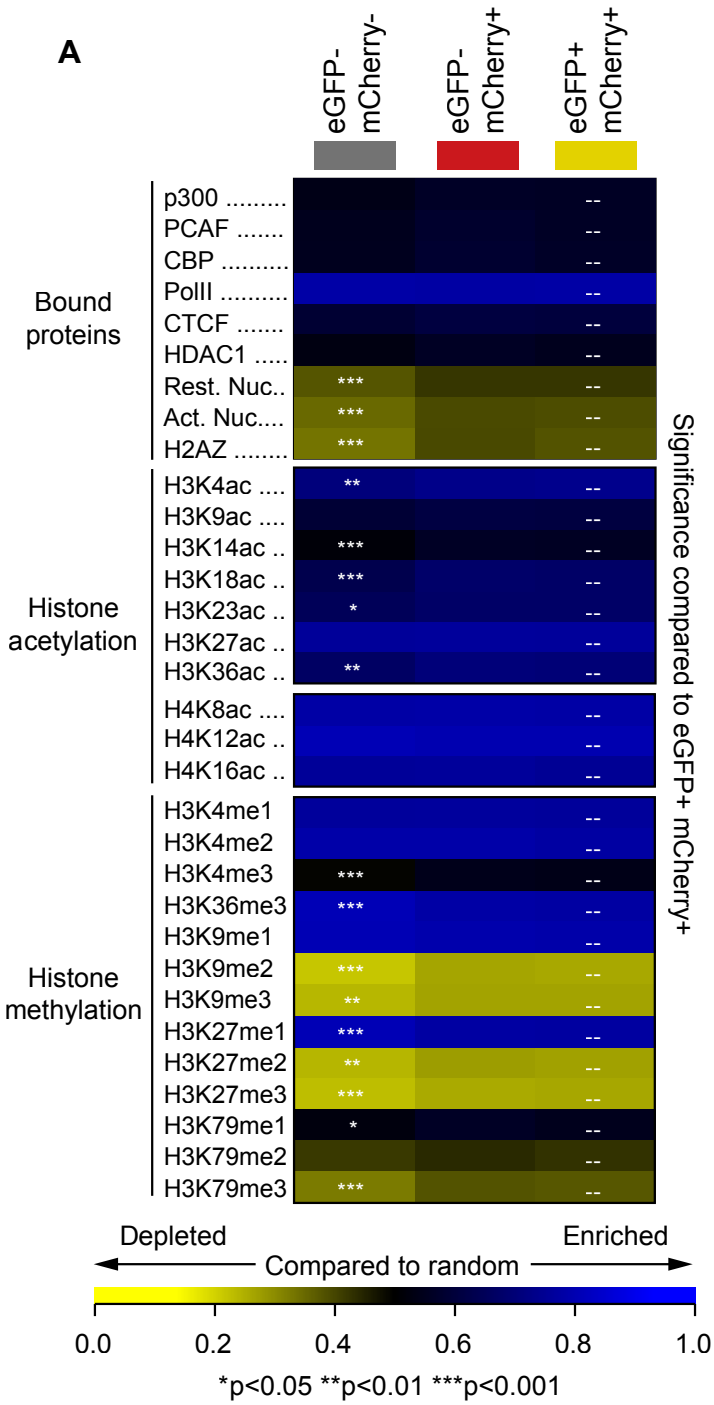
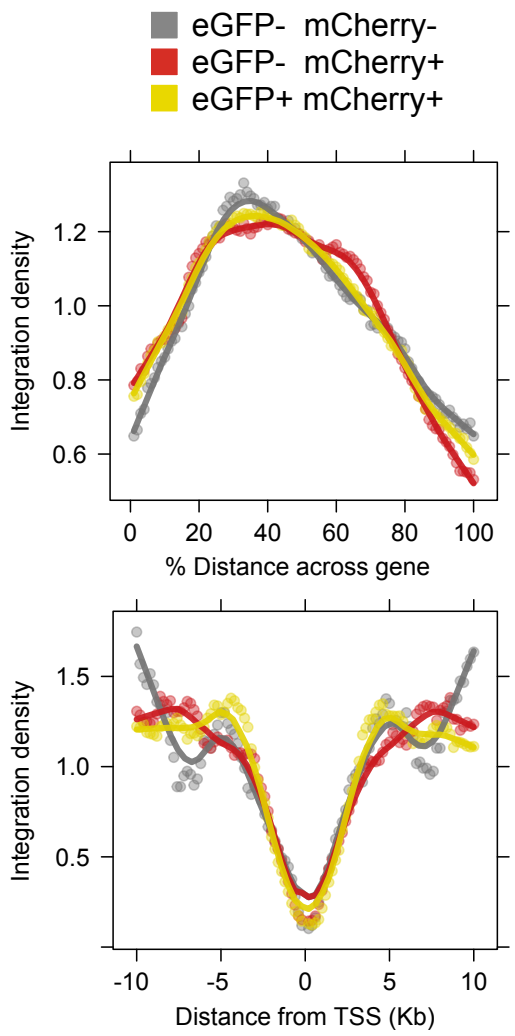
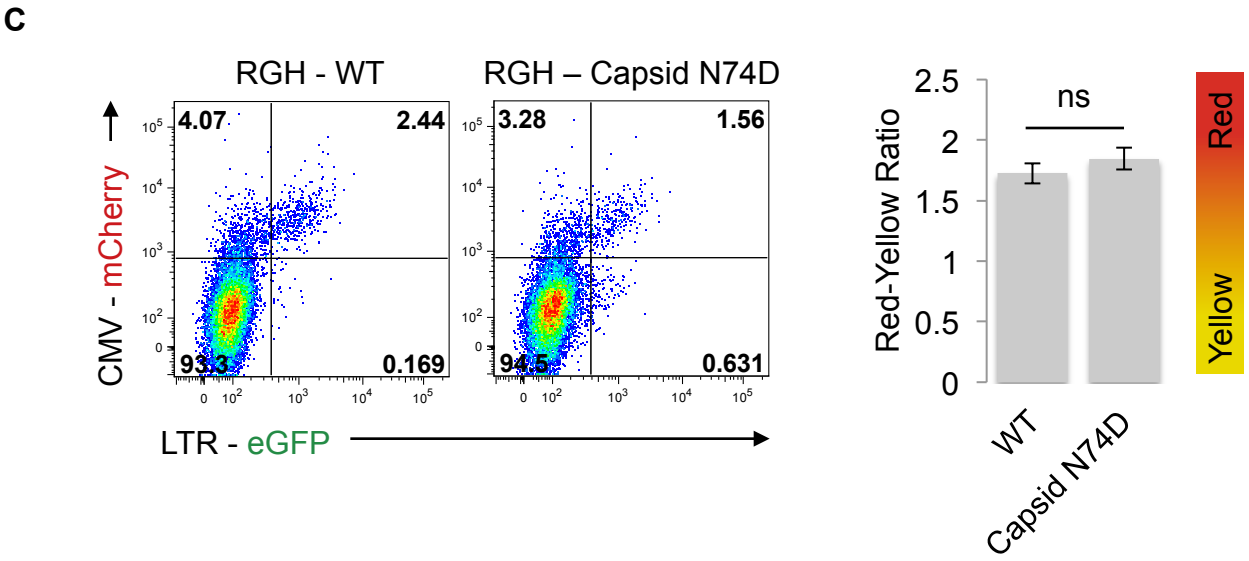
Figure S1


A
eGFP- mCherry-
eGFP- mCherry+
eGFP+ mCherry+
Bound proteins
p300
PCAF
CBP
PolII
CTCF
HDAC1
Rest. Nuc.
Act. Nuc.
H2AZ
Histone acetylation
H3K4ac
H3K9ac
H3K14ac
H3K18ac
H3K23ac
H3K27ac
H3K36ac
H4K8ac
H4K12ac
H4K16ac
Histone methylation
H3K4me1
H3K4me2
H3K4me3
H3K36me3
H3K9me1
H3K9me2
H3K9me3
H3K27me1
H3K27me2
H3K27me3
H3K79me1
H3K79me2
H3K79me3
Significance compared to eGFP+ mCherry+
Depleted
Enriched
Compared to random
0.0
0.2
0.4
0.6
0.8
1.0
*p<0.05 **p<0.01 ***p<0.001


B
eGFP- mCherry-
eGFP- mCherry+
eGFP+ mCherry+
Integration density
% Distance across gene
Distance from TSS (Kb)


C
RGH - WT
RGH – Capsid N74D
4.07
2.44
93.3
0.169
3.28
1.56
94.5
0.631
CMV - mCherry
LTR - eGFP
Red-Yellow Ratio
ns
Red
Yellow
WT
Capsid N74D